

Amendments to the claims:

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a substantially purified Avilll peptide with cellulase activity and, said Avilll peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme having at least 70 90% identity to SEQ ID NO. 1, said Avilll peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, the catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (Avilll_Aac):

GH74_Ace	ATTOPTTWWVVAICCCG	IVDGLIVPNVSGANPGLLYVRLTDIGCMYRMDAAMGRNIPPLDNWG
Avilll_Aac	AGCQVFTWVAVVTPGSGGFTPGCVVNP8AKVAVARATD	DIGCMVNLMSDDTTTPLDNWG
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GH74_Ace	WVWVGCGVWVGLAABDENTVNVWVAVCMYTNSDPNDGAILR8SDCGATWVTPPLPKLG	
Avilll_Aac	NDTWEDNGIDALATDWDTRDRVWVCMYTNSDPNTVCGILR8TDQGDWTWTTPLPKVG	
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GH74_Ace	CNMPGRGMGSRLLAVDPNNDTLYFCAPGCKGLWRCTDCCATWQOMNTFIDVCTVIANPDD	
Avilll_Aac	CNMPGRGMGSRLLAVDPNQVCLLYFGARSCHGLWKTSDYCATWSNVTSPTWTCTYFQD866	
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GH74_Ace	TPGKQGDGCGVWVAVSDK8886LCCQASXKTFVGVADPNNDPWFWRDCCATWQAVPGAP-T	
Avilll_Aac	TYTSDPVGIAKUTPDETEGCCCCATPRITVGVADACKGVTKGEDAGNTWAVSCERQX	
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GH74_Ace	GPIPKKGVTPDYNHIVVATGCTGCPYDG88CDVWKFATFSCITFTRISPVQESTDANQF	
Avilll_Aac	GPIPKKGVLSPESKTVVIGVANACGPYDGCTNGTVKANITSCWVNDISTP-TOLASTPV	
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GH74_Ace	CYSCLTIDRQHPTNTVAVATGCTWPDTTIPRTDCCATWTRIWTWVSPNRLRVULD8	
Avilll_Aac	CGYCGDVLQNPCTLIVVAVLNCWWDDELIPRSTDSGATWSPINWVNGYFCINPYYCVDIG	
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GH74_Ace	AEPWLTPGVQPNPPVDPGKLCMMDAAMAIIDPFTSDRMLVCTGATLYATNDLTWDGSGQX	
Avilll_Aac	NAPKIQDTSTDQFF-VRVCNVAEALAIIDPFTSDRMLVCTGATLYVGGHDLTWDGSGQX	
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GH74_Ace	SHAPWPKGLEETAVNDLICPPGCAALIGALCDLCCFTADVTAVPSTIFTSPVFTTCTSV	
Avilll_Aac	TVKGLAVGTEEMAVLGLTTPPGCAGLLSAVCDGCPYHSDLDAAAPWQAVHTPTVCTTNGI	
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GH74_Ace	DYAECLNPQIVRAGSTDPGCGQWDRIPVFCGDCCGNNPQCGEPGGVTTGCTVACADGCR	
Avilll_Aac	DYAGCNGPQIVRSGGAGDYP-TLALSGNPOSTWADYIAQSTCTGAVALSADGDT	

GH74_Aac	FWWAPCDPGQDVPPVAVGFCENSWAECGVPANQIQRSDRVAIDKTYFALCNGTPFRCTGGCW
Avilll_Aac	VLLMESTSGALVSKCQC
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GH74_Aac	TPQPVAAQLPSSCAVGVVFLHAAPCKECDLWLAAACSLVCTCTVGGGSGATTCVSSAATV
Avilll_Aac	SPTRKTVGCGSSTTAAIRAHPEIACDVACTDKGLWISTDVCSTTQIGSGVTAGNGCF
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GH74_Aac	CPCGKSAPESSCKPAPVFTCTIGGTCAYRSDDCCTTFLINDDQHGVNNGQNTTCGDHAN
Avilll_Aac	CPCGKASSTGCTVVTCTTIDCAAGLPKSEDACTNWQVLCDAHNPCCGGSANVNGDLET
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GH74_Aac	LRRVWCTNGRCIVVGBIGGAPCC
Avilll_Aac	YCRVFRCHRPCHLRLGCGRBPGC

2. (Previously Presented) The composition of claim 1 wherein the Avilll peptide is further defined as comprising a linker and a signal sequence.

3. (Cancelled)

4. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the Avilll peptide is further defined as comprising a length of about 80 to about 150 amino acids.

5. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the Avilll peptide is further defined as comprising a length of about 90 amino acids.

6. (Previously Presented) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.

7. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.

8. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Previously Presented) The composition of claim 1 wherein said Avilll protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74_Ace has at least 90% sequence identity with SEQ ID NO: 3.

11. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.

12. (Previously Presented) An isolated Avilll peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Previously Presented) An industrial mixture suitable for degrading cellulose, such mixture comprising the Avilll polypeptide of claim 1.

15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[.]

16-27 (Cancelled)

28. (Previously Presented) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;
- c) a polypeptide sequence of SEQ ID NO: 5;
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Presented) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)

47. (New) The composition of claim 1 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII_Aac):

GH74_Ace ATTQPYTWSNVATGGGG - FVDGIVFNEGAPGILYVRTDIDGGMYRWDAAANGRNPILLDWVG
AvIII_Aac AASQAYTWKNNVVTGGGGGFTGIVFNPNSAKGVAYARTDIDGGAIRLNSSD - TWTPLMWDVG

GH74_Ace WNNWGYNGVVSIAADPINTINKWVVAAGMYTNSWDPNDGAILRSSDQGATWQITPLPKLG
AviIII_Aac NOTWHWDWGIDALATDPVDTDRVYAVGMYTNEWDPNVGSIILRSTDQGDTWTEKLPFKVG

GH74_Ace TTGIVQSDIQQVWVAFDKSSSSLGQASKTIVFGVADPNPWFWSRDGGATWQAVPGAP-T
AvIII_Aac ---YTSDFVGIANVTFDSTS\$G\$SATPRIFFGVADAGKSFK\$EDAGATWANVSGEPOY

GH74_Acs
AviIII_Aac

GP1PHKGVPFDPVNVHLVLYIATTSNTGGPYDGS9GDVWKF8VTSGTWRISFVPSTDANDYF
GFLPHKGVLSPPEEKTLYIYSTANGAGPYDGTNGTVHCKYNITSGVWTDISP---TSLA8TYY

GH74_Ace	GYSGLTIDRQHPNTIMVATQISWWPTDIIIFRSTDGGATWTRIWDWT\$PNRSLRYVLDIS
AviIII_Aac	GYGGILSVDLQVPGTLMVAALNCWWPDELIFRSTDGATWSPIWEWNGYPSINYYSYDIS ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	AEPWLTFGVQPNPPVPSPKLGMDEAMAIDPPNSDRMLYGTGATLYATNDLTKWDSCGGQI
AviIII_Aac	NAPWIQDTTSTDQFP--VRVGNMVEALAIDPPDSNHLYGTGLTVYGGHDLTNWDSKHNV ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPPVTTGTSV
AviIII_Aac	TVKSLAVGIEEMAVLGLITPPCGPALLSAVGDDGGFYHSDDAARNQAYHTPTYGTNGI ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	DYAEILNPSIIVRAGSFDPSSQPNDRHVAFSTDGGNNWFOGSEPCGGVITGGTVAAASADGSR
AviIII_Aac	DYAGNPKPSNIVRSGASDYP---TLALSSNPGSTWYADYAASTSTGTGAVALSADGDT ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	PVWAPGDPGQPVVYAVGPGNWSAASQGVPPANAQIRSDRVRNPKTFFYALSGNTFYRSTDGGV
AviIII_Aac	VLLMSSTSGALVSKSQG--TILTAVSSLPSCAVIAISDKSDNTVYGGSAGAIYVSKNTAT ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	TPQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGSSWSAI-TGVSSAVNV
AviIII_Aac	SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTPTQICSGVTAGWSF ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	GFGKSAAPGSSYPAPVVGTTIGGVGTGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac	GFGKASSTGSSYVYGGFTIDCAAGLPKSEDAGTAWQVISDAHGFSGSGSANVUNGDLQT ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	LRRVYIGTNCRGIVYGDIGGAPSG
AviIII_Aac	YGRVFRGHERPGMLLRQSOREPAG ***:***:***:***:***

48. (New) The composition of claim 47 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

49. (New) A composition comprising a substantially purified AviIII peptide having at least 99% identity to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.

50. (New) The composition of claim 49 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII_Aac):

GH74_Ace	ATTQPYTWNSVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGYMYRWDAAANGRWIPLLDWVG
AviIII_Aac	AASQAYTWKNVVTGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	WNNWGYNGVVSIAADPINTNKVWAAGVGMYTNSWDPPNDGAIILRSSDQGATWQITPLPFKLG
AviIII_Aac	NUTWHDNGIDALATDPVTDTRVYVAVGMYTNEWDPNVGSILRSTDQGDTWETKLPPFKVG ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	GNMPGRGMGERLAVDPNNDNLYFGAPSGKGGLWRSTDGATWSQMTNPPDVGTIANPTD
AviIII_Aac	GNMPGRGMGERLAVDPNKNISLYFGARSGHGLWKSSTDGATWSNVTSPWTGTYPQDSS3 *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****

GH74_Ace	TTGYQSDIQGVVVVAFDKSSSSLCQASKTIFVGVADPNNEPVFNSRDGGATWQAVPGAP-T
AviIII_Aac	T--YTSDFVGIAWVTFDSTSGSSGSATPRIFVGVADAGK5VFKESEDAGATWANVSGEPQY
GH74_Ace	GFIPIHKGVFDPVNHVLYIATSNTOGPYDGSSGDWKFSVTSGTWTRISPVPSDTANDYF
AviIII_Aac	GFLPHKGVLSPPEKTLVLYISANGACPYDGTTVHKYNTSGVWTDISP---TSLASTYY
GH74_Ace	GYSGLTIDRQHFNNTIMVATQ1SNNWPDIIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDIS
AviIII_Aac	GYGGLSVLDLQVPGTLMVAALNCNWPDDELIFRSTDGSATWSPINEWNGYP5INYYSYDIS
GH74_Ace	AEPFWLTFCVQFPNPPVPSPKLGWMDDEANAIIDPFNSDRMLYGTGATLYATNDLTWDGGQI
AviIII_Aac	NAPWQDQTTSDDQFP---VRVGMVDEALAIIDPFDSNHLYGTGLTVYGGHDLTNWDSKHNV
GH74_Ace	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGPTHADVTAVPSTIFTSPVFTTGT6V
AviIII_Aac	TVKSLAVGIEEMAVLQLITPPGGPALLSAVGDGGFYHSLDLAPNQAYHTPTYCTTNGI
GH74_Ace	DYAEELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKQNWFGSEPGGVTGGTVAAASADGSR
AviIII_Aac	DYAGNKPSNIVRSGASDDYP---TLALSNPGSTWYADYAASTSTGTGAVALSADGDT
GH74_Ace	FVWAPGDPGQPVYYAVCPGNNSWAASQGVPAQIRSDRVNPKTFYALSNGTPYRSTDGGV
AviIII_Aac	VLLMSSTSGALVSKQG---TLTAVSSLPSCAVIASDKSDNTVYCGSAGAYXSKNTAT
GH74_Ace	TFQPVAAAGLPSSGAVGVMFHAVPGKEGDLWLAAS8GLYHSTNGSSWSAI-TGVSSAVNV
AviIII_Aac	SFTKTVS-LGSSTTVNAIR-AMPSIAGDVWASTDKGLWHSTDYGSTPTQIGSGVTAGWSF
GH74_Ace	GPGKSAPGSSYPAVFVVGTTIGGTGAYRSDDCGTTWVLINDDQMQYGN-WGQAITGDHAN
AviIII_Aac	GFGKASSSTG5YVVIYGFFTIDGAAGLFKSEDAQTNWQVISDASHGFGSGSANVNGDLQT
GH74_Ace	LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac	YGRVFRGKMERPGHLLRQSQRREPAG

51. (New) The composition of claim 50 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

52. (New) A composition comprising a substantially purified AviIII peptide having an amino acid sequence identical to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.

53. (New) A composition comprising a substantially purified AviIII peptide, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain GH74_Ace having a sequence that is at least 90% identical to SEQ ID NO. 3.

54. (New) The composition of claim 51 wherein said catalytic domain
GH74_Ace has a sequence identical to SEQ ID NO. 3.